

What is claimed is :

1. A method for introducing a foreign DNA of interest into a preselected site of a genome of a plant cell comprising the steps of
  - (a) inducing a double stranded DNA break at the preselected site in the genome of the cell ;
  - (b) introducing the foreign DNA of interest into the plant cell ;characterized in that the foreign DNA is delivered by direct DNA transfer.
2. The method of claim 1 wherein said direct DNA transfer is accomplished by bombardment of microprojectiles coated with the foreign DNA of interest.
3. The method of claim 1 or 2, wherein said foreign DNA of interest is flanked by a DNA region having at least 80% sequence identity to a DNA region flanking the preselected site.
4. The method of any one of claims 1 to 3, wherein said double stranded DNA break is induced by introduction of a I-SceI encoding gene.
5. The method of claim 4 wherein said I-SceI encoding gene comprises a nucleotide sequence encoding the amino acid sequence of SEQ ID No 1, wherein said nucleotide sequence has a GC content of about 50% to about 60%, provided that
  - vii) said nucleotide sequence does not comprise a nucleotide sequence selected from the group consisting of GATAAT, TATAAA, AATATA, AATATT, GATAAA, AATGAA, AATAAG, AATAAA, AATAAT, AACCAA, ATATAA, AATCAA, ATACTA, ATAAAAA, ATGAAA, AAGCAT, ATTAAT, ATACAT, AAAATA, ATTAAA, AATTAA, AATACA and CATAAA;
  - viii) said nucleotide does not comprise a nucleotide sequence selected from the group consisting of CCAAT, ATTGG, GCAAT and ATTGC;
  - ix) said nucleotide sequence does not comprise a sequence selected from the group consisting of ATTAA, AAGGT, AGGTA, GGTA or GCAGG;

- x) said nucleotide sequence does not comprise a GC stretch consisting of 7 consecutive nucleotides selected from the group of G or C;
  - xi) said nucleotide sequence does not comprise a AT stretch consisting of 5 consecutive nucleotides selected from the group of A or T; and
  - xii) said nucleotide sequence does not comprise the codons TTA, CTA, ATA, GTA, TCG, CCG, ACG and GCG.
6. The method of claim 5, wherein the I-SceI encoding gene comprises the nucleotide sequence of SEQ ID 4.
7. The method of any of the foregoing claims, whereby the plant cell is a maize cell.
8. The method of claim 7, wherein the maize cell is comprised within a cell suspension.
9. The method of any of the foregoing claims, whereby said plant cell is incubated in a plant phenolic compound prior to step a).
10. The method of claim 9, wherein said plant phenolic compound is acetosyringone.
11. A method for introducing a foreign DNA of interest into a preselected site of a genome of a plant cell comprising the steps of
  - (a) inducing a double stranded DNA break at the preselected site in the genome of the cell ;
  - (b) introducing the foreign DNA of interest into the plant cell ;characterized in that the double stranded DNA break is introduced by a rare cutting endonuclease encoded by a nucleotide sequence wherein said nucleotide sequence has a GC content of about 50% to about 60%, provided that
  - i) said nucleotide sequence does not comprise a nucleotide sequence selected from the group consisting of GATAAT, TATAAA, AATATA, AATATT, GATAAA, AATGAA, AATAAG, AATAAA, AATAAT, AACCAA, ATATAA, AATCAA,

ATACTA, ATAAAA, ATGAAA, AAGCAT, ATTAAT, ATACAT, AAAATA, ATTAAA, AATTAA, AATACA and CATAAA;

- ii) said nucleotide does not comprise a nucleotide sequence selected from the group consisting of CCAAT, ATTGG, GCAAT and ATTGC;
- iii) said nucleotide sequence does not comprise a sequence selected from the group consisting of ATTAA, AAGGT, AGGTA, GGTA or GCAGG;
- iv) said nucleotide sequence does not comprise a GC stretch consisting of 7 consecutive nucleotides selected from the group of G or C;
- v) said nucleotide sequence does not comprise a AT stretch consisting of 5 consecutive nucleotides selected from the group of A or T; and
- vi) said nucleotide sequence does not comprise the codons TTA, CTA, ATA, GTA, TCG, CCG, ACG and GCG.

12. The method of claim 11, wherein the nucleotide sequence comprises the nucleotide sequence of SEQ ID 4.

13. The method of claim 11 or 12, wherein the foreign DNA of interest is introduced into said plant cell by direct DNA transfer.

14. The method of any one of claims 11 to 13, wherein said direct DNA transfer is accomplished by bombardment of microprojectiles coated with the foreign DNA of interest.

15. The method of any one of claims 11 to 14, wherein said foreign DNA of interest is flanked by a DNA region having at least 80% sequence identity to a DNA region flanking the preselected site.

16. The method of any one of claims 11 to 15, wherein said double stranded DNA break is induced by introduction of a I-SceI encoding gene.

17. The method of any of the foregoing claims, whereby the plant cell is a maize cell.

18. The method of claim 17, wherein the maize cell is comprised within a cell suspension.
19. The method of any of the foregoing claims, whereby said plant cell is incubated in a plant phenolic compound prior to step a).
20. The method of claim 19, wherein said plant phenolic compound is acetosyringone.
21. A method for introducing a foreign DNA of interest into a preselected site of a genome of a plant cell comprising the steps of
  - (a) inducing a double stranded DNA break at the preselected site in the genome of the cell ;
  - (b) introducing the foreign DNA of interest into the plant cell ;characterized in that prior to step a, the plant cells are incubated in a plant phenolic compound.
22. The method according to claim 21, wherein said plant phenolic compound is selected from the group of acetosyringone (3,5-dimethoxy-4-hydroxyacetophenone), α-hydroxyacetosyringone, sinapinic acid (3,5 dimethoxy-4-hydroxycinnamic acid), syringic acid (4-hydroxy-3,5 dimethoxybenzoic acid), ferulic acid (4-hydroxy-3-methoxycinnamic acid), catechol (1,2-dihydroxybenzene), p-hydroxybenzoic acid (4-hydroxybenzoic acid), β-resorcylic acid (2,4 dihydroxybenzoic acid), protocatechuic acid (3,4-dihydroxybenzoic acid), pyrogallic acid (2,3,4 -trihydroxybenzoic acid), gallic acid (3,4,5-trihydroxybenzoic acid) and vanillin (3-methoxy-4-hydroxybenzaldehyde).
23. A method for introducing a foreign DNA of interest into a preselected site of a genome of a plant cell comprising the steps of
  - (a) inducing a double stranded DNA break at the preselected site in the genome of the cell by a rare cutting endonuclease ;
  - (b) introducing the foreign DNA of interest into the plant cell ;characterized in that said endonuclease comprises a nuclear localization signal.

24. An isolated DNA fragment comprising a nucleotide sequence encoding the amino acid sequence of SEQ ID No 1, wherein the nucleotide sequence has a GC content of about 50% to about 60%, provided that

- i) said nucleotide sequence does not comprise a nucleotide sequence selected from the group consisting of GATAAT, TATAAA, AATATA, AATATT, GATAAA, AATGAA, AATAAG, AATAAA, AATAAT, AACCAA, ATATAA, AATCAA, ATACTA, ATAAAA, ATGAAA, AAGCAT, ATTAAT, ATACAT, AAAATA, ATTAAA, AATTAA, AATACA and CATAAA;
- ii) said nucleotide does not comprise a nucleotide sequence selected from the group consisting of CCAAT, ATTGG, GCAAT and ATTGC;
- iii) said nucleotide sequence does not comprise a sequence selected from the group consisting of ATTTA, AAGGT, AGGTA, GGTA or GCAGG;
- iv) said nucleotide sequence does not comprise a GC stretch consisting of 7 consecutive nucleotides selected from the group of G or C;
- v) said nucleotide sequence does not comprise a AT stretch consisting of 5 consecutive nucleotides selected from the group of A or T; and
- vi) codons of said nucleotide sequence coding for Leu, Ile, Val, Ser, Pro, Thr, Ala do not comprise TA or GC duplets in positions 2 and 3 of said codons.

25. An isolated DNA fragment comprising the nucleotide sequence of SEQ ID No 2, wherein the GC content of said nucleotide sequence is about 50 to about 60%, provided that

- i) said nucleotide sequence from position 28 to position 30 is not AAG;
- ii) if the nucleotide sequence from position 34 to position 36 is AAT then the nucleotide sequence from position 37 to position 39 is not ATT or ATA;
- iii) if the nucleotide sequence form position 34 to position 36 is AAC then the nucleotide sequence from position 37 to position 39 is not ATT simultaneously with the nucleotide sequence from position 40 to position 42 being AAA;
- iv) if the nucleotide sequence from position 34 to position 36 is AAC then the nucleotide sequence from position 37 to position 39 is not ATA;

- v) if the nucleotide sequence from position 37 to position 39 is ATT or ATA then the nucleotide sequence from position 40 to 42 is not AAA;
- vi) the nucleotide sequence from position 49 to position 51 is not CAA;
- vii) the nucleotide sequence from position 52 to position 54 is not GTA;
- viii) the codons from the nucleotide sequence from position 58 to position 63 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise ATTTA;
- ix) if the nucleotide sequence from position 67 to position 69 is CCC then the nucleotide sequence from position 70 to position 72 is not AAT;
- x) if the nucleotide sequence from position 76 to position 78 is AAA then the nucleotide sequence from position 79 to position 81 is not TTG simultaneously with the nucleotide sequence from position 82 to 84 being CTN;
- xi) if the nucleotide sequence from position 79 to position 81 is TTA or CTA then the nucleotide sequence from position 82 to position 84 is not TTA;
- xii) the nucleotide sequence from position 88 to position 90 is not GAA;
- xiii) if the nucleotide sequence from position 91 to position 93 is TAT, then the nucleotide sequence from position 94 to position 96 is not AAA;
- xiv) if the nucleotide sequence from position 97 to position 99 is TCC or TCG or AGC then the nucleotide sequence from position 100 to 102 is not CCA simultaneously with the nucleotide sequence from position 103 to 105 being TTR;
- xv) if the nucleotide sequence from position 100 to 102 is CAA then the nucleotide sequence from position 103 to 105 is not TTA;
- xvi) if the nucleotide sequence from position 109 to position 111 is GAA then the nucleotide sequence from 112 to 114 is not TTA;
- xvii) if the nucleotide sequence from position 115 to 117 is AAT then the nucleotide sequence from position 118 to position 120 is not ATT or ATA;
- xviii) if the nucleotide sequence from position 121 to 123 is GAG then the nucleotide sequence from position 124 to position 126;
- xix) the nucleotide sequence from position 133 to 135 is not GCA;
- xx) the nucleotide sequence from position 139 to position 141 is not ATT;

- xxi) if the nucleotide sequence from position 142 to position 144 is GGA then the nucleotide sequence from position 145 to position 147 is not TTA;
- xxii) if the nucleotide sequence from position 145 to position 147 is TTA then the nucleotide sequence from position 148 to position 150 is not ATA simultaneously with the nucleotide sequence from position 151 to 153 being TTR;
- xxiii) if the nucleotide sequence from position 145 to position 147 is CTA then the nucleotide sequence from position 148 to position 150 is not ATA simultaneously with the nucleotide sequence from position 151 to 153 being TTR;
- xxiv) if the nucleotide sequence from position 148 to position 150 is ATA then the nucleotide sequence from position 151 to position 153 is not CTA or TTG;
- xxv) if the nucleotide sequence from position 160 to position 162 is GCA then the nucleotide sequence from position 163 to position 165 is not TAC;
- xxvi) if the nucleotide sequence from position 163 to position 165 is TAT then the nucleotide sequence from position 166 to position 168 is not ATA simultaneously with the nucleotide sequence from position 169 to position 171 being AGR;
- xxvii) the codons from the nucleotide sequence from position 172 to position 177 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise GCAGG;
- xxviii) the codons from the nucleotide sequence from position 178 to position 186 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise AGGTA;
- xxix) if the nucleotide sequence from position 193 to position 195 is TAT, then the nucleotide sequence from position 196 to position 198 is not TGC;
- xxx) the nucleotide sequence from position 202 to position 204 is not CAA;
- xxxi) the nucleotide sequence from position 217 to position 219 is not AAT;
- xxxii) if the nucleotide sequence from position 220 to position 222 is AAA then the nucleotide sequence from position 223 to position 225 is not GCA;
- xxxiii) if the nucleotide sequence from position 223 to position 225 is GCA then the nucleotide sequence from position 226 to position 228 is not TAC;

- xxxiv) if the nucleotide sequence from position 253 to position 255 is GAC, then the nucleotide sequence from position 256 to position 258 is not CAA;
- xxxv) if the nucleotide sequence from position 277 to position 279 is CAT, then the nucleotide sequence from position 280 to position 282 is not AAA;
- xxxvi) the codons from the nucleotide sequence from position 298 to position 303 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise ATTTA;
- xxxvii) if the nucleotide sequence from position 304 to position 306 is GGC then the nucleotide sequence from position 307 to position 309 is not AAT;
- xxxviii) the codons from the nucleotide sequence from position 307 to position 312 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise ATTTA;
- xxxix) the codons from the nucleotide sequence from position 334 to position 342 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise ATTTA;
- xl) if the nucleotide sequence from position 340 to position 342 is AAG then the nucleotide sequence from position 343 to 345 is not CAT;
- xli) if the nucleotide position from position 346 to position 348 is CAA then the nucleotide sequence from position 349 to position 351 is not GCA;
- xlii) the codons from the nucleotide sequence from position 349 to position 357 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise ATTTA;
- xliii) the nucleotide sequence from position 355 to position 357 is not AAT;
- xliv) if the nucleotide sequence from position 358 to position 360 is AAA then the nucleotide sequence from position 361 to 363 is not TTG;
- xlv) if the nucleotide sequence from position 364 to position 366 is GCC then the nucleotide sequence from position 367 to position 369 is not AAT;
- xlvi) the codons from the nucleotide sequence from position 367 to position 378 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise ATTTA;

- xlvii) if the nucleotide sequence from position 382 to position 384 is AAT then the nucleotide sequence from position 385 to position 387 is not AAT;
- xlviii) the nucleotide sequence from position 385 to position 387 is not AAT;
- xlix) if the nucleotide sequence from position 400 to 402 is CCC, then the nucleotide sequence from position 403 to 405 is not AAT;
- i) if the nucleotide sequence from position 403 to 405 is AAT, then the nucleotide sequence from position 406 to 408 is not AAT;
- ii) the codons from the nucleotide sequence from position 406 to position 411 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise ATTTA;
- iii) the codons from the nucleotide sequence from position 421 to position 426 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise ATTTA;
- liii) the nucleotide sequence from position 430 to position 432 is not CCA;
- liv) if the nucleotide sequence from position 436 to position 438 is TCA then the nucleotide sequence from position 439 to position 441 is not TTG;
- lv) the nucleotide sequence from position 445 to position 447 is not TAT;
- lvi) the nucleotide sequence from position 481 to 483 is not AAT;
- lvii) if the nucleotide sequence from position 484 to position 486 is AAA, then the nucleotide sequence from position 487 to position 489 is not AAT simultaneously with the nucleotide sequence from position 490 to position 492 being AGY;
- lviii) if the nucleotide sequence from position 490 to position 492 is TCA, then the nucleotide sequence from position 493 to position 495 is not ACC simultaneously with the nucleotide sequence from position 496 to 498 being AAY;
- lix) if the nucleotide sequence from position 493 to position 495 is ACC, then the nucleotide sequence from position 496 to 498 is not AAT;
- lx) the nucleotide sequence from position 496 to position 498 is not AAT;
- lxi) if the nucleotide sequence from position 499 to position 501 is AAA then the nucleotide sequence from position 502 to position 504 is not TCA or AGC;

- lxii) if the nucleotide sequence from position 508 to position 510 is GTA, then the nucleotide sequence from position 511 to 513 is not TTA;
- lxiii) if the nucleotide sequence from position 514 to position 516 is AAT then the nucleotide sequence from position 517 to position 519 is not ACA;
- lxiv) if the nucleotide sequence from position 517 to position 519 is ACC or ACG, then the nucleotide sequence from position 520 to position 522 is not CAA simultaneously with the nucleotide sequence from position 523 to position 525 being TCN;
- lxv) the codons from the nucleotide sequence from position 523 to position 531 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise ATTTA;
- lxvi) if the nucleotide sequence from position 544 to position 546 is GAA then the nucleotide sequence from position 547 to position 549 is not TAT, simultaneously with the nucleotide sequence from position 550 to position 552 being TTR;
- lxvii) the codons from the nucleotide sequence from position 547 to position 552 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise ATTTA;
- lxviii) if the nucleotide sequence from position 559 to positon 561 is GGA then the nucleotide sequence from position 562 to position 564 is not TTG simultaneously with the nucleotide sequence from position 565 to 567 being CGN;
- lxix) if the nucleotide sequence from position 565 to position 567 is CGC then the nucleotide sequence from position 568 to position 570 is not AAT;
- lxx) the nucleotide sequence from position 568 to position 570 is not AAT;
- lxxi) if the nucleotide sequence from position 574 to position 576 is TTC then the nucleotide sequence from position 577 to position 579 is not CAA simultaneously with the nucleotide sequence from position 580 to position 582 being TTR;
- lxxii) if the nucleotide sequence from position 577 to position 579 is CAA then the nucleotide sequence from position 580 to position 582 is not TTA;
- lxxiii) if the nucleotide sequence from position 583 to position 585 is AAT the the nucleotide sequence from position 586 to 588 is not TGC;

- lxxiv) the nucleotide sequence from position 595 to position 597 is not AAA;
- lxxv) if the nucleotide sequence from position 598 to position 600 is ATT then the nucleotide sequence from position 601 to position 603 is not AAT;
- lxxvi) the nucleotide sequence from position 598 to position 600 is not ATA;
- lxxvii) the nucleotide sequence from position 601 to position 603 is not AAT;
- lxxviii) if the nucleotide sequence from position 604 to position 606 is AAA then the nucleotide sequence from position 607 to position 609 is not AAT;
- lxxix) the nucleotide sequence from position 607 to position 609 is not AAT;
- lxxx) the nucleotide sequence from position 613 to position 615 is not CCA;
- lxxxi) if the nucleotide sequence from position 613 to position 615 is CCG, then the nucleotide sequence from position 616 to position 618 is not ATA;
- lxxxii) if the nucleotide sequence from position 616 to the nucleotide at position 618 is ATA, then the nucleotide sequence from position 619 to 621 is not ATA;
- lxxxiii) if the nucleotide sequence from position 619 to position 621 is ATA, then the nucleotide sequence from position 622 to position 624 is not TAC;
- lxxxiv) the nucleotide sequence from position 619 to position 621 is not ATT;
- lxxxv) the codons from the nucleotide sequence from position 640 to position 645 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise ATTTA;
- lxxxvi) if the nucleotide sequence from position 643 to position 645 is TTA then the nucleotide sequence from position 646 to position 648 is not ATA;
- lxxxvii) if the nucleotide sequence from position 643 to position 645 is CTA then the nucleotide sequence from position 646 to position 648 is not ATA;
- lxxxviii) the codons from the nucleotide sequence from position 655 to position 660 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise ATTTA;
- lxxxix) if the nucleotide sequence from position 658 to 660 is TTA or CTA then the nucleotide sequence from position 661 to position 663 is not ATT or ATC;
- xc) the nucleotide sequence from position 661 to position 663 is not ATA;

- xci) if the nucleotide sequence from position 661 to position 663 is ATT then the nucleotide sequence from position 664 to position 666 is not AAA;
  - xcii) the codons from the nucleotide sequence from position 670 to position 675 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise ATTTA;
  - xciii) if the nucleotide sequence from position 691 to position 693 is TAT then the nucleotide sequence from position 694 to position 696 is not AAA;
  - xciv) if the nucleotide sequence from position 694 to position 696 is AAA then the nucleotide sequence from position 697 to position 699 is not TTG;
  - xcv) if the nucleotide sequence from position 700 to position 702 is CCC then the nucleotide sequence from position 703 to position 705 is not AAT;
  - xcvi) if the nucleotide sequence from position 703 to position 705 is AAT then the nucleotide sequence from position 706 to position 708 is not ACA or ACT;
  - xcvii) if the nucleotide sequence from position 706 to position 708 is ACA then the nucleotide sequence from position 709 to 711 is not ATA simultaneously with the nucleotide sequence from position 712 to position 714 being AGY;
  - xcviii) said nucleotide sequence does not comprise the codons TTA, CTA, ATA, GTA, TCG, CCG, ACG and GCG;
  - xcix) said nucleotide sequence does not comprise a GC stretch consisting of 7 consecutive nucleotides selected from the group of G or C; and
- c) said nucleotide sequence does not comprise a AT stretch consisting of 5 consecutive nucleotides selected from the group of A or T.

26. An isolated DNA fragment comprising the nucleotide sequence of SEQ ID No 3 wherein the GC content of said nucleotide sequence is about 50 to about 60%, provided that
- a) if the nucleotide sequence from position 121 to position 123 is GAG then the nucleotide sequence from position 124 to 126 is not CAA;
  - b) if the nucleotide sequence from position 253 to position 255 is GAC then the nucleotide sequence from position 256 to 258 is not CAA;

- c) if the nucleotide sequence from position 277 to position 279 is CAT then the nucleotide sequence from position 280 to 282 is not AAA;
- d) if the nucleotide sequence from position 340 to position 342 is AAG then the nucleotide sequence from position 343 to position 345 is not CAT;
- e) if the nucleotide sequence from position 490 to position 492 is TCA then the nucleotide sequence from position 493 to position 495 is not ACC;
- f) if the nucleotide sequence from position 499 to position 501 is AAA then the nucleotide sequence from position 502 to 504 is not TCA or AGC;
- g) if the nucleotide sequence from position 517 to position 519 is ACC then the nucleotide sequence from position 520 to position 522 is not CAA simultaneous with the nucleotide sequence from position 523 to 525 being TCN;
- h) if the nucleotide sequence from position 661 to position 663 is ATT then the nucleotide sequence from position 664 to position 666 is not AAA;
- i) the codons from the nucleotide sequence from position 7 to position 15 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise a stretch of seven contiguous nucleotides from the group of G or C;
- j) the codons from the nucleotide sequence from position 61 to position 69 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise a stretch of seven contiguous nucleotides from the group of G or C;
- k) the codons from the nucleotide sequence from position 130 to position 138 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise a stretch of seven contiguous nucleotides from the group of G or C;
- l) the codons from the nucleotide sequence from position 268 to position 279 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise a stretch of seven contiguous nucleotides from the group of G or C;
- m) the codons from the nucleotide sequence from position 322 to position 333 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise a stretch of seven contiguous nucleotides from the group of G or C;

- n) the codons from the nucleotide sequence from position 460 to position 468 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise a stretch of seven contiguous nucleotides from the group of G or C;
- o) the codons from the nucleotide sequence from position 13 to position 27 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise a stretch of five contiguous nucleotides from the group of A or T;
- p) the codons from the nucleotide sequence from position 37 to position 48 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise a stretch of five contiguous nucleotides from the group of A or T;
- q) the codons from the nucleotide sequence from position 184 to position 192 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise a stretch of five contiguous nucleotides from the group of A or T;
- r) the codons from the nucleotide sequence from position 214 to position 219 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise a stretch of five contiguous nucleotides from the group of A or T;
- s) the codons from the nucleotide sequence from position 277 to position 285 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise a stretch of five contiguous nucleotides from the group of A or T;
- t) the codons from the nucleotide sequence from position 388 to position 396 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise a stretch of five contiguous nucleotides from the group of A or T;
- u) the codons from the nucleotide sequence from position 466 to position 474 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise a stretch of five contiguous nucleotides from the group of A or T;
- v) the codons from the nucleotide sequence from position 484 to position 489 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise a stretch of five contiguous nucleotides from the group of A or T;
- w) the codons from the nucleotide sequence from position 571 to position 576 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise a stretch of five contiguous nucleotides from the group of A or T;

- x) the codons from the nucleotide sequence from position 598 to position 603 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise a stretch of five contiguous nucleotides from the group of A or T;
  - y) the codons from the nucleotide sequence from position 604 to position 609 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise a stretch of five contiguous nucleotides from the group of A or T;
  - z) the codons from the nucleotide sequence from position 613 to position 621 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise a stretch of five contiguous nucleotides from the group of A or T;
- aa) the codons from the nucleotide sequence from position 646 to position 651 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise a stretch of five contiguous nucleotides from the group of A or T;
  - bb) the codons from the nucleotide sequence from position 661 to position 666 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise a stretch of five contiguous nucleotides from the group of A or T; and
  - cc) the codons from the nucleotide sequence from position 706 to position 714 are chosen according to the choices provided in such a way that the resulting nucleotide sequence does not comprise a stretch of five contiguous nucleotides from the group of A or T.
27. An isolated DNA sequence according to claim 26, characterized in that it contains a nucleotide sequence differing from the nucleotide sequence of SEQ ID No 4 in only one position.
28. An isolated DNA sequence according to claim 26, characterized in that it contains a nucleotide sequence differing from the nucleotide sequence of SEQ ID No 4 in only ten positions.
29. An isolated DNA sequence comprising the nucleotide sequence of SEQ ID No 4.

30. A chimeric gene comprising the isolated DNA fragment according to any one of claims 24 to 29 operably linked to a plant-expressible promoter.
31. Use of a chimeric gene according to claim 30 to insert a foreign DNA into an I-SceI recognition site in the genome of a plant.